

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 17:42:19 ; Search time 23 seconds

(Without alignments)
732.147 Million cell updates/sec

Title: US-09-782-587b-1

Perfect score: 2187
Sequence: 1 ANAFELXXRPGSLXRXCKXX.....LQKLRSEPRGVLLRPF 406

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match	Length	ID	Description
1	2167	99.1	466	FA7_HUMAN	P08709 homo sapien
2	1634.5	74.7	444	FA7_RABIT	P98139 oryctolagus
3	1567.5	71.7	446	FA7_MOUSE	P70375 bos musc
4	1566	71.6	407	FA7_BOVIN	P22457 bos taurus
5	858.5	39.3	475	FA10_CHICK	P25155 gallus gall
6	858.5	39.3	488	FA10_HUMAN	P00742 homo sapien
7	850.5	38.9	416	FA9_BOVIN	P00741 bos taurus
8	849	38.8	461	FA9_HUMAN	P00740 homo sapien
9	843.5	38.6	490	FA10_RABIT	P019045 oryctolagus
10	843	38.5	492	FA10_BOVIN	P00743 bos taurus
11	824	37.7	459	FA9_MOUSE	P16294 mus muscu
12	821	37.5	452	FA9_CANFA	P19540 canis fami
13	786.5	36.0	459	PRIC_PIG	Q991P2 sus scrofa
14	775	35.4	461	PRIC_PIG	P31394 ratius norv
15	769	35.2	461	PRIC_MOUSE	P33587 mus muscu
16	760	34.8	376	FA10_TROCA	P81428 tropidochis
17	749	34.2	456	PRIC_BOVIN	P00745 bos taurus
18	743	34.0	458	PRIC_RABIT	Q28661 oryctolagus
19	726	33.2	461	PRIC_HUMAN	P04070 homo sapien
20	519.5	23.8	275	FA9_RABIT	P16292 oryctolagus
21	515.5	23.6	281	FA9_RAT	P16296 ratius norv
22	513.5	23.5	271	FA9_PIG	P16293 sus scrofa
23	511	23.4	285	FA9_CAVPO	P16295 cavia porce
24	509.5	23.3	274	FA9_SHEEP	P16291 ovis aries
25	473	21.6	638	KAL_MOUSE	P26262 mus muscu
26	463.5	21.2	653	HGRF_MOUSE	Q91098 mus muscu
27	461.5	21.1	638	KAL_RAT	P14772 ratius norv
28	459.5	21.0	638	KAL_HUMAN	P03952 homo sapien
29	445.5	20.4	343	PS8_HUMAN	P16651 homo sapien
30	444	20.3	625	FA11_HUMAN	P03951 homo sapien
31	443.5	20.3	342	PS8_RAT	Q96887 ratius norv
32	443.5	20.3	622	THRB_HUMAN	P00734 homo sapien
33	442	20.2	342	PS8_MOUSE	Q96881 mus muscu

34	439.5	20.1	655	1	HQFA_HUMAN	Q04756 homo sapien
35	439.5	20.1	1069	1	ENTK_MOUSE	P97435 mus muscu
36	428.5	19.6	625	1	THRB_BOVIN	P00735 bos taurus
37	428	19.6	1035	1	ENTK_BOVIN	P98072 bos taurus
38	426.5	19.5	246	1	TRY1_RAT	P00762 ratius norv
39	425.5	19.5	618	1	THRB_MOUSE	P19221 mus muscu
40	423	19.3	229	1	TRYP_SODAC	P00764 squallus aca
41	423	19.3	492	1	TMS2_HUMAN	O15393 homo sapien
42	421	19.3	617	1	THRB_RAT	P18282 ratius norv
43	420.5	19.2	247	1	TRY3_RAT	P08426 ratius norv
44	419.5	19.2	416	1	HEPS_MOUSE	O35453 mus muscu
45	418	19.1	1019	1	ENTK_HUMAN	P98073 homo sapien

ALIGNMENTS

RESULT 1
FA7_HUMAN
ID FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709: 014339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
DE F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
vitamin K-dependent protein participating in blood coagulation";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi O., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
factor VIIa from plasma and transfected baby hamster kidney cells";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Moberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
glycosylations at serine residues 52 and 60 and effects of site-
directed mutagenesis of serine 52 to alanine";
RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shionishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein z and bovine protein z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE-91344709; PubMed-2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE-96175641; PubMed-8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE-99126538; PubMed-9925787;
 RA Zhang E., St Charles R., Tullinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE-96367502; PubMed-9692950;
 RA Mutanyi A., Finn B.E., Gipeert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE-91300046; PubMed-2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE-93340074; PubMed-1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE-93372811; PubMed-8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE-94061028; PubMed-8242057;
 RA Takamizu O., Kembai-Cook G., Marin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE-94264305; PubMed-8204879;
 RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE-95072589; PubMed-7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MET HIS-307.
 RX MEDLINE-95064662; PubMed-7974346;
 RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CNC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE-96247510; PubMed-8652821;
 RA Arblin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283, K-325, V-358, Q-364, E-402 AND Q-413.
 RX MEDLINE-97001216; PubMed-8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE-97037613; PubMed-8883260;
 RA Temary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zalzov R., Seligson U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE-98112461; PubMed-9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aguilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [22]
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC [23]
 RP CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-Ile bond in factor X to
 CC form factor Xa.
 CC [24]
 RP SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC [25]
 RP ALTERNATIVE PRODUCTS: 2 isoforms: A (shown here) and B; are
 CC produced by alternative splicing.
 CC [26]
 RP TISSUE SPECIFICITY: PLASMA.
 CC [27]
 RP PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC [28]
 RP DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC [29]
 RP PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match	71.7%	Score	1567.5	DB	1	Length	446
Best Local Similarity	68.1%	Pred. No.	4.8e-115				
Matches	275	Conservative	46	Mismatches	15	Indels	1
						Gaps	1

```

RESULT 4
FEA7_BOVIN
FEA7_BOVIN
P22457;
01-AUG-1991 (Rel. 19; Created)
01-AUG-1991 (Rel. 19; last sequence update)
15-JUN-2002 (Rel. 41; last annotation update)
Coagulation factor VII (EC 3.4.21.21) (Serum
prothrombin conversion
accelerator).
F7.
GN

```

Iakeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,

RA	Iwanaga S.;
RT	"Bovine factor VII. Its purification and complete amino acid sequence."
RL	J. Biol. Chem.
RN	263:14868-14877(1988).
[2]	
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.
RX	MEDLINE=8921399; PubMed=3145637;
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA	Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
RT	A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RL	J. Biochem.
RN	104:867-868(1988).
[3]	
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.
RX	MEDLINE=91344709; PubMed=2129376;
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel M., Hase S., Ikenaka T.
RT	"A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";
RL	Adv. Exp. Med. Biol.
CC	281:121-133(1990).
-1-	FUNCTION: CIRCULATES IN THE BLOOD IN A DYMOMEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
-1-	CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-Ile bond in factor X to form factor xa.
-1-	SUBUNIT: HEMERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
-1-	TISSUE SPECIFICITY: PLASMA.
-1-	PTM: THE VITAMIN K-DEPENDENT, ENZYMTATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-1-	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1-	SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	PIR: A31979; A31979.
DR	HSP, P08709; IBF9.
DR	MEROPS; S01_215; -
DR	Interpro: IPRO00152; Asx_hydroxy1.
DR	Interpro: IPRO0314; Chymotrypsin.
DR	Interpro: IPRO00561; EGF-like.
DR	Interpro: IPRO00742; EGF-2.
DR	Interpro: IPRO01861; EGF-Ca.
DR	Interpro: IPRO01438; EGF-II.
DR	Interpro: IPRO02383; Gln_blood.
DR	Interpro: IPRO01254; Ser_protase-Try.
DR	Interpro: IPRO00294; Vitk_dep_GLA.
DR	pfam: PF00008; EGF_2.
DR	pfam: PF00089; trypsin; 1.
DR	pfam: PF00594; gla; 1.
DR	PRINTS: PR00722; CHYMOTRYPSIN.
DR	PRINTS: PRO0010; EGFBLOOD.
DR	PRINTS: PRO0001; GLABLOOD.
DR	SMART: SM00179; EGF_CA_1.
DR	SMART: SM00001; EGF_Like_1.
DR	SMART: SM00069; GLA; 1.
DR	SMART: SM00020; TRYP_SPC; 1.
DR	PROSITE: PS00010; ASX_HYDROXYL; 1.
DR	PROSITE: PS00022; EGF_1; 1.
DR	PROSITE: PS01186; EGF-2; 2.
DR	PROSITE: PS01187; EGF_CA_1.
DR	PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE: PS00240; TRYPSIN_DOM; 1.
DR	PROSITE: PS00134; TRYPSIN_HTS; 1.
DR	PROSITE: PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease; Blood coagulation; zymogen; glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxylutamic acid; EGF-like domain; Repeat.
FT	CHAIN
ET	1
FT	CHAIN
ET	153
FT	DOMAIN
ET	6
FT	DOMAIN
ET	46
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152
FT	CHAIN
ET	407
FT	DOMAIN
ET	35
FT	DOMAIN
ET	128
FT	DOMAIN
ET	82
FT	DOMAIN
ET	87
FT	DOMAIN
ET	152

Query Match	71.6%	Score 1566	DB 1	Length 407
Best Local Similarity	69.6%	Pred. No. 5.7e-115		
Matches 27/5	Conservative 45	Mismatches 75	Indels 0	Gaps 0
QY	1	ANAFXXLRPGSLXRXCKXXQCSFXAXRIFPKAXRTKLFWISYSDGDCCASSPCONGGS	60	
Db	1	ANGFLEELLPGSLERECREELCSFEAEHIEPRNEERTROFWVSYNDDQCCASSPCONGGS	60	
QY	61	CNDOLOSYCFCLPAFEGGRNETHKHDOOLIVANNNGCCBOYCSDPHTGTRKSCCHGYSI	120	
Db	61	CEDQURSYICEPDPFEGGRNCEYKQSOGLICANNGCCBOYCSADPAGRFCWCHGYSAL	120	
QY	121	LADGVSCTPTVEYPCGKIPILEKRNASAPGGRITGVGKRCGEGPQWVULLVNGAOLCG	180	
Db	121	QADGVSCTPTVEYPCGKIPYLEKRNKSGPGRITGVGHVCPGEGPQWVAMKLKGLCG	180	
QY	181	TLINTIWWVSAAHCEBDKIKMWRNLIAYLGEHDLSEHGDQCSRRVAQVITPSTYVEGTN	240	
Db	181	TLAGVWVSAAHCEPERLSRSGNLTAYLGEHDLSEHGDQCSRRVAQVITPSTYVEGTN	240	
QY	241	HDIALRLHOPVVLTDHYVPLCLDEPRFSEPTLAFVPSLSVSGMQLLDGATALELAVL	300	
Db	241	HDVALLQALQAPVALLGDHYAPLCLDPDPFADDTLAFVPSVSGMQLLDEGATVARKLAVV	300	
QY	301	IVPRILMTDQCLQOOSRKVDSPNITREYFEGAGYSPGSDSCGSGGPHAHNYGTYVLG	360	
Db	301	LVPRILMTDQCLQOOSRKVDSPNITREYFEGAGYSPGSDSCGSGGPHAHNYGTYVLG	360	
QY	361	IYVSGGQCATVGHGEGVTVRVSOYIEMLQKLMRSEP	395	
Db	361	IYVSGGQCATVGHGEGVTVRVSOYIEMLQKLMRSEP	395	

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE (Virus activating protease) (VAP).
GN FX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianineae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Chorioallantoic membrane;
RC MEDLINE=91257322; PubMed=2044767;
RX Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotch B.,
RA Ogasawara T., Nagai Y.,
RA "Primary structure of the virus-activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa.",
RL FEBS Lett. 283:281-285(1991).
[2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RX MEDLINE=91065352; PubMed=2174359;
RA Gotch B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,
RA Nagai Y.,
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo.",
RL EMO J. 9:4189-4195(1990).
[1] FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
converts prothrombin to thrombin in the presence of factor Va,
calcium and phospholipid during blood clotting.
[1] FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
SAC.
[1] CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
Arg-|-Ile bonds in prothrombin to form thrombin.
[1] SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
MORE DISULFIDE BONDS.
[1] TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
[1] PM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CALCIUM.
[1] PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
[1] SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
[1] SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00844; BAA00724.1; -
DR PIR; S15838; S15838.
DR HSSP; P00742; 1HCG.
DR MEROPS; S01.216; -
DR InterPro; IPR000152; Asx_hydroxy1.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-11ke.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001841; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PRO0010; EGFBLD.
 DR SMART; PRO0001; GLABLOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF-1; 1.
 DR PROSITE; PS01186; EGF-2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 OR 30, OR 31 (POTENTIAL).
 FT PROPEP 1 20
 FT CHAIN 21 40
 FT CHAIN 41 180
 FT PROPEP 186 475
 FT CHAIN 186 475
 FT CHAIN 242 475
 FT DOMAIN 86 122
 FT DOMAIN 125 168
 FT DOMAIN 241 475
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 FT MOD_RES 66 66
 FT MOD_RES 69 69
 FT MOD_RES 72 72
 FT MOD_RES 79 79
 FT MOD_RES 103 103
 FT ACT_SITE 282 328
 FT ACT_SITE 328 328
 FT ACT_SITE 425 425
 FT DISULFID 90 101
 FT DISULFID 95 110
 FT DISULFID 112 121
 FT DISULFID 129 140
 FT DISULFID 136 152
 FT DISULFID 154 167
 FT DISULFID 175 348
 FT DISULFID 247 252
 FT DISULFID 267 283
 FT DISULFID 396 410
 FT DISULFID 421 449
 FT CARBOHYD 196 196
 FT CARBOHYD 207 207
 FT CARBOHYD 228 228
 FT CARBOHYD 285 285
 FT SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;

Query Match 39.3%; Score 858.5; DB 1; Length 475;
 Best Local Similarity 37.3%; Pred. No. 9.3e-60;

Matches 167; Conservative 76; Mismatches 138; Indels 67; Gaps 8;

1 ANAFLXLRPGSLKRXKXKXCCSFXXARXIRKDAYRTRFLFWISYSDGDCASPCONGGS 60

OY

Db 41 ANSFLERKOGNIERECNEERCSKEAREAFEDNEXTEEFMNIVYDGDCCSPCHYGGQ 100
 OY 61 CKDQLOSYICFCIPABGRNCEFHKKDQL---CVNENGCEBOYCSDHGTGRS--CRGH 115
 Db 101 CKDGLSYTCSCLDYOGKNCFE---VIPKYCKINNGCEBOFCISIKRSVKDVCSCST 155
 OY 116 EGYSLADGVSCTPYVEYPCGKI-----PILEKRNASKPGC----- 151
 Db 156 SGTELEADGKQCSKRYKPCGKVLKRIKRSVLLPTNSNTNATSDDDVPSTNGSILEEYF 215
 OY 152 -----RIVGKVCPCGCEPMQ-VLLVNGAQLCGTLINTI 186
 Db 216 TTTESPTPEPRNGSSITDPNVDTIRIVGDECPGSCPMQAVLINKEGFEFCGTLIND 275
 OY 187 WVSANAHCEDKINNMNLAVLGEHDLSEHDGDEOSRRVAQVIIPSTYPGTTNHDIAL 246
 Db 276 FILTAHACINQSK---EIKVYGEVDREKESEHETHTAEKIFVHSKYIAETVNDIALI 332
 OY 247 RLHPVYVLDHYVPLCLPTEFSERTLAFVRSFLVSGMGOLDRGATALEVLVAVPRLM 306
 Db 333 KLEKEPQFSEYVYVACLPADPANEVLMNOKSGWVSGFEREEAGLSRLVLEVPYVD 392
 OY 307 TDDCLQOSRKRYGDSPIITEYMFCAYSDSKDSCKGSGCPATHYRGTWYLTGIYSWCO 366
 Db 393 RSTCKQSTNFA-----ITEMFCAGYETEQKDACGDSGPHYTRKDYFTVGIYSWCE 447
 OY 367 GCATVGHFVYRVVSYIEMLOKMARSE 394
 Db 448 GCARKGKRYGVYTKLSRFLRMVRYVMROK 475

RESULT 6

FA10_HUMAN STANDARD; PRT; 488 AA.
 ID P00742; Q14340;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP MEDLINE-91216473; PubMed-1902434;
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 human coagulation factor X.";
 RT Gene 99:291-294(1991).
 RN [2]
 RP MEDLINE-87026600; PubMed-3768336;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 organization is essentially identical with that of factor IX and
 protein C.";
 RT Biochemistry 25:5098-5102(1986).
 RN [3]
 RP MEDLINE-85216545; PubMed-2582420;
 RA Fung W.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 blood coagulation factor X.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-86221713; PubMed-3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood coagulation factor X

RT "Isolation and characterization of human factor IX cDNA:
RT Identification of Tag I polymorphism and regional assignment.";
RL Somat. Cell Mol. Genet. 10:465-473(1984).
RN [6]
RX SEQUENCE OF 290-359 FROM N.A.
RX MEDLINE-88127096; PubMed-3340835;
RX Stoffel E.S., Koebel D.D., Sarkar G., Sommer S.S.;
RT "Genomic amplification with transcript sequencing.";
RL Science 239:491-494(1988).
RN [7]
RP SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE-94054330; PubMed-8236150;
RX de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,
RX Wiesel M.L., Grunbaum L., Gazeave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
RT gene responsible for mild haemophilia B.";
RL Thromb. Haemost. 70:370-371(1993).
RN [8]
RP SEQUENCE OF 47-461 (VARIANT NAGOVA).
RX MEDLINE-90078229; PubMed-2592373;
RX Suenhiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RX Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell
RT chymase.";
RL J. Biol. Chem. 264:21257-21265(1989).
RN [9]
RP HYDROXYLATION OF ASP-110.
RX MEDLINE-83308813; PubMed-6688526;
RX McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [10]
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-78194509; PubMed-659613;
RX di Scipio R.G., Kunitachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor).";
RL J. Clin. Invest. 61:1528-1538(1978).
RN [11]
RP CALCIUM-BINDING DATA.
RX MEDLINE-84185715; PubMed-6425296;
RX Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RT "Derivatives of blood coagulation factor IX contain a high affinity
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
RL J. Biol. Chem. 259:5698-5704(1984).
RN [12]
RP ERRATUM.
RX Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RL J. Biol. Chem. 260:2383-2583(1985).
RN [13]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE-86189947; PubMed-3009023;
RX Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
RT "Defective propeptide processing of blood clotting factor IX caused
RT by mutation of arginine to glutamine at position -4.";
RL Cell 45:343-348(1986).
RN [14]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE-90062160; PubMed-2511201;
RX Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RX Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein 2 and bovine protein 2.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [15]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE-91344709; PubMed-2129367;
RX Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein 2.";

RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [16]
RP STRUCTURE OF CARBOHYDRATE ON SER-107.
RX MEDLINE-92388094; PubMed-1517205;
RX Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RT serine 61 through the fucose residue.";
RL J. Biol. Chem. 267:17520-17525(1992).
RN [17]
RP PHOSPHORYLATION OF SER-114.
RX Harris R.O., Papac D.I., Tyuong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";
RL (in) Abstracts of XIth International conference on methods in protein
RL structure analysis, pp.50-50, Annecy (1996).
RN [18]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE-20573597; PubMed-11133752;
RX Arruda V.R., Hagstrom J.N., Deitch J., Helman-Patterson T.,
RX Camhre R.M., Chu K., Fiedle P.A., Herzog R.W., Couto L.B.,
RT "Posttranslational modifications of recombinant myotube-synthesized
RT human factor IX.";
RL Blood 97:130-138(2001).
RN [19]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-95229607; PubMed-7713897;
RX Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
RT binding region of factor IX by two-dimensional NMR spectroscopy.";
RL J. Biol. Chem. 270:7980-7987(1995).
RN [20]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-96032604; PubMed-7547952;
RX Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RT domain of factor IX.";
RL Biochemistry 34:12126-12137(1995).
RN [21]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-96279169; PubMed-8663165;
RX Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
RX Furie B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RT dependent blood coagulation protein factor IX.";
RL J. Biol. Chem. 271:16227-16236(1996).
RN [22]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-97199336; PubMed-9047312;
RX Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RX Smith H., Hiskey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RT gamma-carboxyglutamic acid domain of coagulation factor IX using
RT molecular dynamics simulation with initial Ca2+ positions determined
RT by a genetic algorithm.";
RL Biochemistry 36:2132-2138(1997).
RN [23]
RP STRUCTURE BY NMR OF 91-133.
RX MEDLINE-91308127; PubMed-1854745;
RX Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney M.V.;
RT "Sequence-specific 1H NMR assignments, secondary structure, and
RT location of the calcium binding site in the first epidermal growth
RT factor like domain of blood coagulation factor IX.";
RL Biochemistry 30:7402-7409(1991).
RN [24]
RP STRUCTURE BY NMR OF 92-130.
RX MEDLINE-93284090; PubMed-1304885;
RX Barton M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RX Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RT human factor IX: comparison with EGF and TGF-alpha.";
RL Protein Sci. 1:81-90(1992).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.

Query Match	38.6%	Score 843.5	DB 1	Length 450
Best local Similarity	37.9%	Pred. No. 1.4e-58		
Matches 168	Conservative 79	Mismatches 137	Indels 59	Gaps 9

Query Match	38.68;	Score 843.5;	DB 1;	Length 490;
Best Local Similarity	37.98;	Pred No 1	4e-58.	

Matches 168; Conservative 79; Mismatches 137; Indels 59; Gaps 9

QY 1 ANAFLXLHPGSLXRCKKXQCSFXXARXIFKDAKTKLEWISYSDGDQACASSPCQNGS 60

Db

41 ANSFLEELKGNLERECBEENCSYEALVEYFEDREKTNEEWNKYYDSDFSPBICNOGT 100

61 CKDQLOSICGLPAFFGRNCE--THKDDQICVNENGGCEGVASCDNMCMKTRKCDQDINQAV 110

[illegible][illegible]

```

119 SLADGVSCPTVEYPCGKIPLEKR-----NSK--PQG----- 151
:::| | | :|||: | |:|: |

```

D_b 156 TLGDNGKSCISTELFP CGKYTLGRWRRSPAIN_SSEGPPEAPCGPEQDDGNLTAT_ETENP_NL 215

07 152 -----RIVGKVC PKGECPPVOYLL-VNGAQLCGTLLINIVVSAHC 194

Db 216 LDSPEPPEDSSSLVRIVGQDCRDGECPQALLVNEENEGECGTTLSHYHTAAHC 275

195 FDKIKNMRNLIAVLGEHDLSEHDGDEOSRBRVAOVITPSTYVPGTNNHIALI.PIHORYI 254

```

      : | ::          :|: |   :||:: | |: | : |||:||| : 
276 LHOAKREK---VPRVCDDPTTEHFEENFETUUTGIVTUVLUNRITUMVTVDSTATIGCAGGGGTGGC 300

```

[illegible]

```

253 IDHVFELCPERIFSERI LAFVRFSLVSGSGQLDGRGATALEMVLNVPRILMTQDCLQOS 314
      :| ||:: :: || : ::||:: :| :|::| :| :|

```

333 RANVAPACLPQKDMAESTLMAQKTGIVSGFGRTHEMGRSLSTTLKMLEVYVDNRNSCKRSS 392

315 RKVGDSPNITEYMFACAGISDGSCKDCKDGGPHATHYRGWYLTGIIVSWGQCATVGHF 374

Db 393 -----SFTITQNMFCAGYDARPEDACQGSBGGPHVTRFRDITYEVTGLVSWGEGCARKGKF 447

QY 375 GYTRVSQYIENLQKLMRSEPRP 397

448 GVTYKVSNFLKWKIEKSMRARVP 470

RESULT 10
DATA POINT

FA10_BOVIN	FA10_BOVIN	STANDARD;	PRT;	492 AA.
ID	FA10_BOVIN			

AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)

DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)

Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).

Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RA MEDLINE=84247315; PubMed-6330671;
RX Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RL containing a prepro leader sequence.";
RN Nucleic Acids Res. 12:4481-4492(1984).
RN (2)
RN SEQUENCE OF 41-180.
RA MEDLINE=80130563; PubMed-6766735;
RX Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RL factor).";
RN Biochemistry 19:659-667(1980).
RN (3)
RN REVISION TO 103.
RA MEDLINE=83308813; PubMed-6688526;
RX McKullen B.A., Fujikawa K., Kistel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RL K-dependent blood coagulation zymogens.";
RN Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN (4)
RN SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RA MEDLINE=76031069; PubMed-1059093;
RX Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RL chain.";
RN Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN (5)
RN SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RA MEDLINE=94062825; PubMed-8243461;
RX Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RL peptides of blood coagulation factor X. The role of the carbohydrate
RN moieties in the activation of factor X.";
RN Eur. J. Biochem. 218:153-163(1993).
RN (6)
RN ACTIVE SITE.
RA MEDLINE=73053314; PubMed-4264286;
RX Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
RN with mammalian serine proteases.";
RN Biochemistry 11:4899-4903(1972).
RN (7)
RN PROCESSING.
RA MEDLINE=76053121; PubMed-1059122;
RX Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RN Xa-alpha to factor Xa-beta.";
RN Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN (8)
RN CALCIUM-BINDING DATA.
RA MEDLINE=84185716; PubMed-6546930;
RX Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RN carboxyglutamic acid-containing region.";
RN J. Biol. Chem. 259:5705-5710(1984).
RN (9)
RN SOLVENTION.
RA MEDLINE=86140210; PubMed-3949800;
RX Morita T., Jackson C.M.;
RT "Localisation of the structural difference between bovine blood
RN coagulation factors XI and X2 to tyrosine 18 in the activation
RN peptide.";
RN J. Biol. Chem. 261:4008-4014(1986).
RN (10)

[illegible]


```

Db 46 GNLRECIETEEECSEEAEREVEENTETETFEWKQYVDGQCESNCLNGIGKIDKDISSEEC 105
Qy 71 FCLPAFGRCNCEHKKDQLICVNGGCEQYCSHTGTKSCREHGYSLADGVSCTPT 130
Db 106 WCVGFGRCNEL----DATCNINNGRCOKFCNKNPDKNYCSCTEGYLAEDKSCSEPT 161
Qy 131 VEPGCKRPT-----LEKRNASKP 149
Db 162 VPFCGRASISYSKRTTRAEVPSNMDYENSTFAVEIODDITDGLNNTVSESESLND 221
Qy 150 OGRVGVKCPKCEKPCPOVILLNGAOLCGTLINTVWSAHCFF---DKIKMRNLIA 206
Db 222 FTRVGVGNKPKQIPQWVILNGEIEAFCGAIIENEKWIYTAANCLPKGKIE-----V 275
Qy 207 VLGEHDLSEHDGDSQSRVAQVILPSTVPGCTN---HDALALLIOPVYLTDHVPCL 263
Db 276 VAEKYNIDKKEDEDRNRNVRT-IPHQYNATINKXSHDLALLLELDPKLINSVYPICV 334
Qy 264 PERTFSERTLAFFRF--SLVSGNGQLDRGATALALMLVNLVPRMLNODCLOQSRKVGDSP 321
Db 335 ANR---EYTNIFLKFSGYSGVSGKVPENKGRHSLIOYLNVPLVDNATCLR-----ST 384
Qy 322 NITEY--MCGAGISDSKSDCKSDSGPNAHYRGTYLIGIVSGCGATVGFYGYTR 379
Db 385 TFFTYYNMCAGYREGKDSCEGDSGPHVTEGTSFLGLISWGECECMKRGKGYTR 444
Qy 380 VSOYEMLOK 389
Db 445 VSRVYMWIKE 454

RESULT 12
FA9_CANFA STANDARD: PRT; 452 AA.
ID FA9_CANFA
AC P19540;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN 11]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=90311364; PubMed=2367529;
RA Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;
RT "Phenotypic correction of factor IX deficiency in skin fibroblasts of
RL hemophilic dogs.",
RL Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990)..
RN 12]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC TISSUE=Liver;
RA MEDLINE=89323338; PubMed=2752110;
RA Evans J.P., Weitzke H.H., Ware J.L., Stafford D.W., High K.A.;
RT "Molecular cloning of a cDNA encoding canine factor IX.",
RL Blood 74:207-212(1989).
RN 13]
RN VARIANT HEMOPHILIA B GLU-418.
RA MEDLINE=9009303; PubMed=2481310;
RA Evans J.P., Brinkhous K.M., Brayer G.D., Relsner H.M., High K.A.;
RT "Canine hemophilia B resulting from a point mutation with unusual
RL consequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
CC IONS, PHOSPHOLIPIDS, AND FACTOR VIII.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.

```

```

FT  MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
FT  MOD_RES 66 66 (BY SIMILARITY).
FT  MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT  MOD_RES 69 69 (BY SIMILARITY).
FT  MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID
FT  MOD_RES 72 72 (BY SIMILARITY).
FT  MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT  MOD_RES 75 75 (BY SIMILARITY).
FT  MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID
FT  MOD_RES 79 79 (BY SIMILARITY).
FT  MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
FT  MOD_RES 103 103 (BY SIMILARITY).
FT  MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT  DISULFID 57 62 (BY SIMILARITY).
FT  DISULFID 90 101 (BY SIMILARITY).
FT  DISULFID 95 110 (BY SIMILARITY).
FT  DISULFID 112 121 (BY SIMILARITY).
FT  DISULFID 127 138 (BY SIMILARITY).
FT  DISULFID 134 148 (BY SIMILARITY).
FT  DISULFID 150 163 (BY SIMILARITY).
FT  CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  ACT_SITE 258 258 CHARGE RELAY SYSTEM.
FT  ACT_SITE 306 306 CHARGE RELAY SYSTEM.
FT  ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT  VARIANT 418 418 G -> E (IN-HEMOPHILIA B).
SQ  SEQUENCE 452 AA: 50827 MW: 1F6537CA6A6960ED CRC64;

Query Match 37.5% Score 821: DB 1: Length 452:
Best Local Similarity 39.5% Pred. No. 7.4e-57:
Matches 165: Conservative 67: Mismatches 133: Indels 50: Gaps 10:

11 GSLKRXKXKXOCSEFXARXIFKDAKRTLEWISYSDGQCSAPQNGSGCKDOLQSYIC 70
51 GNLEECIEECSEFEAREVENTEKTEFEKQYVDGQCCSNCLNDGVCKDDINSTEC 110
71 FCLPAFEGRCNCFKRDQDLICVANGGCEQYCSHDTGKRSCHGEGYSLADVSCPT 130
111 WCRAGFEKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 166
131 VEPFCGKIPKIPKIPKIPKIPKIPKIPKIPKIPKIPKIPKIPKIPKIPKIPKIP 161
167 VPPPCGKVSVPKISMTKRAETLESNMDYENSTEVEKLDVNTOPLDNFTVVGKDKAP 226
162 GECPOVLLLVNGAQLCGGLTINTIWWVSAACPD-KIKMNRNDIAVGEHDLSEHDE 220
227 GQPPMAYLLNGKVDACFCGSGIINEKVVYTAHCIEPOVK-----ITIVAGEINTEKREHTE 282
221 OSRRVAVOVIIPSTY--VPGTTNHDIALRLHQPVLVDHVVPLCLPERTSEETLAIFYR 278
283 OKRNVIRFTILHSHSYNATINKYNHDIALLLEDEPLTNSYVPICIADREYSN--IFLKF 339
279 --SLVSGMGQLDRGATALEMLVNPRLMTQDLOOSRKAKGSDPNITEVFCAGYSGS 336
340 GSGVYSMGKVPFKNGRSASILQYLKVLVDRAITLRSKTFK-----TIYNNFCAGFHEGG 394
337 KDSCKGSDGPHATHTHYGTLYLTGIVMSGGACATVGHGVYTRVSOXIEMLOK 389
395 KDSCKGSDGSGPHYTEVGEISFLTGIIISMGECAMKAKGKIGITTKSRVYNNWIK 447

```

```

RESULT 13
PRTG_PIG STANDARD; PRT: 459 AA.
AC 09GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
PROC.

```

```

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.
RT Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domains.
RT Cell. Mol. Life Sci. 58:148-159(2001).
CC -1 FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1 CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1 SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1 TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1 PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -1 MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC site is necessary for the recognition of the
CC thrombin-thrombomodulin complex.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1 SIMILARITY: CONTRAINS 2 EGF-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.1sb-slb.ch/announce/
CC or send an email to license@1sb-slb.ch).
CC
DR EMBL: AF191307; AAC28380.1; -
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_CA.
DR InterPro: IPR001254; Set_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; Tryp_spc_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1_1.
DR PROSITE: PS01186; EGF_2_2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS0240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPSIN_HIS_1.
DR PROSITE: PS00135; TRYPSIN_SER_1.
DR Blood coagulation; Glycoprotein; Serine protease;
DR Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.

```

```

FT SIGNAL 1 18 BY SIMILARITY.
FT PROPER 19 41 BY SIMILARITY.
FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY
FT CHAIN 199 459 SIMILARITY).
FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY
FT CHAIN 199 459 SIMILARITY).
FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY
FT SITE 213 214 SIMILARITY).
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT DOMAIN 214 459 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 48 48 SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 55 55 SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 57 57 SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 60 60 SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 61 61 SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 66 66 SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 67 67 SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 225 225 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 36.0%; Score 786.5; DB 1; Length 459;
Best Local Similarity 39.4%; Pred No. 3.7e-54;
Matches 166; Conservative 65; Mismatches 151; Indels 39; Gaps 11;

```

```

DB 277 KNEVDIDIEFLVHPNVTSTSDNDIALRLAPATFSOTIVPICPDSLSERELTRVG 336
QY 277 RESVSGMQLDORGTALEMLVNL---VPRLTQDCLQDSRRVGDSPNTEWFCAGS 333
QY 337 QETVTVGMKYSRSE--AKTRNSFLNFIKYPVAPAHNECVQAMNH-----KISEMMLCAGIL 389
DB 334 DSKSDCKDSCGDPNATHYRGTYWLTGIVSMGCGATVGHFGVYTVESQVIEWLOKLMRS 393
QY 390 GDSRDACEGDSGCPMVASFRGTWELVGLVSMGEGCRLNHYGVTVYSRLDMTHIGHIRN 449
QY 394 E 394
DB 450 E 450

RESULT 14
PRTC_RAT 461 AA.
ID PRTC_RAT STANDARD: PRT: 461 AA.
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
DE PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Mistar; TISSUE=Liver;
RA MEDLINE=92329550; PubMed=1627650;
RT Okafuji T., Mekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RT Biochim. Biophys. Acta 1131:329-332(1992).
RL -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS. WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sb.ch/announce/
CC or send an email to license@isb-sb.ch).
CC
CC EMBL; X64336; CAA45617.1;
CC PIR; S18994; S18994.
CC PIR; S24312; S24312.
CC HSRP; P04070; 1PCU.
CC MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.

```

DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser-protease_Try.
 DR InterPro: IPR000294; Vitr_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_1like_1.
 DR SMART: SM00063; GLA_1.
 DR SMART: SM00020; tryp-Spc_1.
 DR PROSITE: PS0010; ASX_HYDROXYL_1.
 DR PROSITE: PS0186; EGF_2_1.
 DR PROSITE: PS0182; EGF_2_2.
 DR PROSITE: PS0187; EGF_CA_1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPsin_DOM_1.
 DR PROSITE: PS00134; TRYPsin_HIS_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 DR Blood coagulation: Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; signal.
 FT SIGNAL 1 32
 FT PROPEP 1 32
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 70 70
 FT ACT_SITE 112 112
 FT ACT_SITE 234 234
 FT ACT_SITE 300 300
 FT ACT_SITE 402 402
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 110
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 320
 FT DISULFID 239 255
 FT DISULFID 373 387
 FT DISULFID 398 426
 FT CARBOHYD 215 215
 FT CARBOHYD 291 291
 FT CARBOHYD 355 355
 FT SEQUENCE 461 AA; 51912 MW; 844CF93664EDACD5 CRC64;

Query Match 35.4%; Score 775; DB 1; Length 461;
 Best Local Similarity 37.7%; Pred. No. 2.9e-53;
 Matches 164; Conservative 67; Mismatches 156; Indels 48; Gaps 11;
 1 ANAFLLXLRPGSLRXXKXQCSFXXARXIFKDAKTKLFWISYSDGDCAS-----52
 42 ANSFLEVRAGSLERFCMEIDCFEAGQEIFQVDETLAFWIKYFGDGCSTPPLDHOD 101
 53 SPQNGSCSKDLOSLICFLPAFEGRNCETHKDDQLICVNGGCEGYCSHTGTGRSC 112
 102 SPCCGHGTCIDIGLGFSCGCDKMGEGRFCCQEWGFG-DCRVKNGCGYHLCLETRGR-C 159
 113 RCHEGXSLADGVSCPTVEYPCGKIPLEKRNASRPG-----RIVG 156
 160 RCPGTELDADHHCPTVNFPGK---LWKTRDKRKKFKKDIDPEDELELGRPIVNG 216
 157 KYCPKGECPMVLVLYNGAQL-CGGTLNTIIVWSAAGFDKIKKRNLTIAVGEHDLSE 215
 217 TLTKQGDSPMAIILDSKKKACGGVLITHSVLTAAHLESSK---KLTVALGEYDLNR 273
 216 HGGDESRVAVYIIPSTYVPGTTHDIALRLHDPVLTDHVPCLLPERTFSERTIAF 275
 274 RDPWEIDLIDKEVLYHPNTRNSNDIDALLRLSDPATLSKTIYPICLPNSGLAQLSQA 333
 276 VRFSLVSGMGLD-----RGATALELVAVNPRIMTODCQOSRKVDSNITETVFC 329
 334 GGEIVYTGNGYSDKVKDGRNRRTFL-LTFIRIPLAARDCKQVNNV---VSENMIC 387
 330 AGYSDGSKDSCGSGGPHATYRGWYLTGIVSGGCAFGVYTRVSQYIEMLOK 389
 388 AGIIGTRDAGCGDSGGPVVFFRGWFLVGLVSGEGCHLNNVGYITKVSYLKWIHS 447
 390 LMRSEPRVLLRAP 404
 448 YIGER---DVSLKSP 459
 RESULT 15
 PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; 035498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP TISSUE=Liver;
 RC MEDLINE=92316697; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=128/SVJ;
 RA MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 RT anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 [3]
 RP SEQUENCE OF 274-434 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;

RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nino Y.;
 RT "A comparative study of partial primary structures of the catalytic
 RL region of mammalian protein C.";
 CC Br. J. Haematol. 86:590-600(1994).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIa.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).
 CC -----
 DR EMBL: D10445; BAA01235.1;
 DR EMBL: AF034569; AAC3795.1;
 DR EMBL: D43755; BAA07812.1;
 DR PIR: JX0210; JX0210.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218;
 DR MGD: MGI:97771; PROC.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00594; glia_1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM000179; EGF_CA; 1.
 DR SMART: SM000001; EGF_Like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_Spe; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT SIGNAL 1 33
 FT PROPEP 34 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).

FT	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	213	461	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	48	48	(BY SIMILARITY).
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	55	55	(BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	57	57	(BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	60	60	(BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	61	61	(BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	66	66	(BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	67	67	(BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	70	70	(BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	112	112	(BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	253	253	CHARGE RELAY SYSTEM.
FT	ACT_SITE	299	299	CHARGE RELAY SYSTEM.
FT	ACT_SITE	402	402	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	(BY SIMILARITY).
FT	DISULFID	91	110	(BY SIMILARITY).
FT	DISULFID	100	105	(BY SIMILARITY).
FT	DISULFID	104	119	(BY SIMILARITY).
FT	DISULFID	121	130	(BY SIMILARITY).
FT	DISULFID	139	150	(BY SIMILARITY).
FT	DISULFID	146	159	(BY SIMILARITY).
FT	DISULFID	161	174	(BY SIMILARITY).
FT	DISULFID	182	319	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	238	254	(BY SIMILARITY).
FT	DISULFID	373	387	(BY SIMILARITY).
FT	DISULFID	398	426	(BY SIMILARITY).
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	328	328	MISSING (IN REF. 2).
FT	CONFLICT	393	393	N -> D (IN REF. 2).
SO	SEQUENCE	461 AA:	51945 MW:	53FAAD85B194D6E CRC64:

Query Match 35.2% Score 769; DB 1; Length 461;
 Best Local Similarity 36.9% Pred. No. 8; 5e-53;
 Matches 159; Conservative 80; Mismatches 150; Indels 42; Gaps 12;

OY	1	ANAFLEXLRPGSLXKCKXKXOCSPXAXXIFRDAARTLFWTISYDGGQAS-----	52
DB	42	ANSFLEEMRPPSLERECEMEICDFEAEQEIFQNVEDTLAFWIKYFDGQCSAPPLDHCQ	101
OY	53	SPCNGSGCKDOLQSYICFCLPAFEGRCNCTHKDQDLICVENGSGCEQCSGHTKSC	112
DB	102	SPCGHGTCIDIGISFSCSKGMRKQCOQLRPQDQRVN-NGCLHYCEESNGR-C	159
OY	113	RCHGYSILADGVSCPTVEYPCGKIP--LEKRNASK-----POGRIVGKVC	160
DB	160	ACAGYELADHMKCKSTVNPCKGLGMIKKRIILRDTLDLEDELPDRIVNGITLK	219
OY	161	KGECPMOVLILVNGAOL-CGGTLLNTIIVVSAANCFDKIKMRNLIAVLGHEHSDHGD	219
DB	220	QGDSPWQITLDSKKKLACGGVLLHTSVVLLAALC---VEGTRKLYRLAGEYDLRRDHW	276
OY	220	EOSRRVAVIIPSTVYVGTWHDIALRLHPVVLTDVHVLCLPERFESRTLAFV-RF	278
DB	277	ELDDDIKELVHPYTRSSSDNDIALRLAPALSLKTIYVICLPNNGLAQDELTOAGOE	336
OY	279	SLVSGWQLD-----RGATALELVANVPRMTODLOOSRKGDSPTTEYFCAGY	332
DB	337	TVYWGMYOSDRIKDGRNRNTEFI-LTFIRIPLVARNBCVEVMKNV-----VSEMLACGI	390
OY	333	SDGSKDCKDSCGPHATHTVLTGIYVSGGCAFTVGHFGVYTRVSOTIEWLQKLMR	392

Db 391 IGNTRDACDGDGSGPMVVFRRGTWFLVGLVSMGECGHTNNYGIYTKVGYLKWIHSYIG 450
OY 393 SEPRGVLLRA 403
Db 451 EK--GVSLKS 458

Search completed: July 1, 2003, 17:52:16
Job time : 25 secs